



## SEQUENCE LISTING

RECEIVED

OCT 16 2003

TECH CENTER 1600/2900

&lt;110&gt; Bruce, Wesley B.

<120> A Nitrate-Responsive Root  
Transcriptional Factor

&lt;130&gt; 1263

&lt;140&gt; US 09/970,624

&lt;141&gt; 2001-10-04

&lt;150&gt; US 60/238,292

&lt;151&gt; 2000-10-05

&lt;160&gt; 3

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 1280

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (360)...(1082)

&lt;400&gt; 1

gcacgagccg ccctgcgcca agaaaagcca tcgttcttcc cacaaacgca cacatagaag 60  
catcattccc ctctcggcta gcttcttccct ctctctccct cctcctcctc ttctcttccc 120  
tcctcccttg ggaaacctgc tgcctttgag ctttcttctt cgagagctcc caccagatct 180  
cctcctcctt accttctttg gcacgttcgg cggcgcgcgc ggagaaagat agatcccgcc 240  
atcgtcgtcg tcggtccttg cttccgatcg gagggccaca accacaacct ctcgctccat 300  
agcgtgcaag cgcgagccag ggtcaagaag agagctagct agctataggc cggagatcg 359  
atg ggg agg gga aag atc gtg atc cgc agg atc gat aac tcc acg agc 407  
Met Gly Arg Gly Lys Ile Val Ile Arg Arg Ile Asp Asn Ser Thr Ser  
1 5 10 15

cgg cag gtg acc ttc tcc aag cgc cgg aac ggg atc ttc aag aag gcc 455  
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala  
20 25 30

aag gag ctc gcc atc ctc tgc gat gcg gag gtc ggc ctc gtc atc ttc 503  
Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Val Ile Phe  
35 40 45

tcc agc acc ggc cgc ctc tac gag tac tct agc acc agc atg aaa tca 551  
Ser Ser Thr Gly Arg Leu Tyr Glu Tyr Ser Ser Thr Ser Met Lys Ser  
50 55 60

gtt ata gat cgg tac ggc aag gcc aag gaa gag cag caa gtc gtc gca 599  
Val Ile Asp Arg Tyr Gly Lys Ala Lys Glu Glu Gln Gln Val Val Ala  
65 70 75 80

aat ccc aac tcg gag ctt aag ttt tgg caa agg gag gca gca agc ttg 647

```

Asn Pro Asn Ser Glu Leu Lys Phe Trp Gln Arg Glu Ala Ala Ser Leu
      85              90              95
aga caa caa ctg cac aac ttg caa gaa aat tat cgg cag ttg acg gga      695
Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly
      100              105              110

gat gat ctt tct ggg ctg aat gtc aaa gaa ctg cag tcc ctg gag aat      743
Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn
      115              120              125

caa ttg gaa aca agc ctg cgt ggt gtc cgc gca aag aag gac cat ctc      791
Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys Asp His Leu
      130              135              140

ttg ata gat gag att cac gat ttg aat cga aag gca agt tta ttt cac      839
Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser Leu Phe His
      145              150              155              160

caa gaa aat aca gac ttg tac aat aag atc aac ctg att cgc caa gaa      887
Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile Arg Gln Glu
      165              170              175

aat gat gag tta cat aaa aag ata tat gag act gaa gga cca agt gga      935
Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly Pro Ser Gly
      180              185              190

gtt aat cgg gag tca ccg act cca ttc aac ttt gca gta gta gaa acc      983
Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val Val Glu Thr
      195              200              205

aga gat gtt cct gtg caa ctt gaa ctc agc aca ctg cca cag caa aat      1031
Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro Gln Gln Asn
      210              215              220

aac att gag cca tct act gct cct aag cta gga ttg caa tta att cca      1079
Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln Leu Ile Pro
      225              230              235              240

tga agaagagtaa aactgccgtc ttatgatgct gaaggaaact atttattgtg      1132
*

aagagatgat actcagagaa agacatatatt gtggcagggga gatttgagat atgaacttat      1192
aaatgtaatg caaataattt tcagaccgga atgggggtcgt ggaattcaga ggatgattgc      1252
tttctaaaaa aaaaaaaaaa aaaaaaaaaa .                                1280

<210> 2
<211> 240
<212> PRT
<213> Zea mays

<400> 2
Met Gly Arg Gly Lys Ile Val Ile Arg Arg Ile Asp Asn Ser Thr Ser
  1          5          10          15
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala
      20              25              30

```

Lys	Glu	Leu	Ala	Ile	Leu	Cys	Asp	Ala	Glu	Val	Gly	Leu	Val	Ile	Phe
	35						40					45			
Ser	Ser	Thr	Gly	Arg	Leu	Tyr	Glu	Tyr	Ser	Ser	Thr	Ser	Met	Lys	Ser
	50					55					60				
Val	Ile	Asp	Arg	Tyr	Gly	Lys	Ala	Lys	Glu	Glu	Gln	Gln	Val	Val	Ala
65					70				75						80
Asn	Pro	Asn	Ser	Glu	Leu	Lys	Phe	Trp	Gln	Arg	Glu	Ala	Ala	Ser	Leu
			85					90						95	
Arg	Gln	Gln	Leu	His	Asn	Leu	Gln	Glu	Asn	Tyr	Arg	Gln	Leu	Thr	Gly
			100					105					110		
Asp	Asp	Leu	Ser	Gly	Leu	Asn	Val	Lys	Glu	Leu	Gln	Ser	Leu	Glu	Asn
	115					120					125				
Gln	Leu	Glu	Thr	Ser	Leu	Arg	Gly	Val	Arg	Ala	Lys	Lys	Asp	His	Leu
	130					135					140				
Leu	Ile	Asp	Glu	Ile	His	Asp	Leu	Asn	Arg	Lys	Ala	Ser	Leu	Phe	His
145					150					155					160
Gln	Glu	Asn	Thr	Asp	Leu	Tyr	Asn	Lys	Ile	Asn	Leu	Ile	Arg	Gln	Glu
			165					170						175	
Asn	Asp	Glu	Leu	His	Lys	Lys	Ile	Tyr	Glu	Thr	Glu	Gly	Pro	Ser	Gly
		180						185					190		
Val	Asn	Arg	Glu	Ser	Pro	Thr	Pro	Phe	Asn	Phe	Ala	Val	Val	Glu	Thr
	195						200					205			
Arg	Asp	Val	Pro	Val	Gln	Leu	Glu	Leu	Ser	Thr	Leu	Pro	Gln	Gln	Asn
	210				215					220					
Asn	Ile	Glu	Pro	Ser	Thr	Ala	Pro	Lys	Leu	Gly	Leu	Gln	Leu	Ile	Pro
225					230					235					240

<210> 3

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 3

tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa